

D475

#2



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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/074,596

DATE: 03/01/2002
TIME: 10:54:34

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3 <110> APPLICANT: ROSENBLUM, MICHAEL G.
 4 CHEUNG, LAWRENCE
 6 <120> TITLE OF INVENTION: MODIFIED PROTEINS, DESIGNER TOXINS, AND METHODS OF
 7 MAKING THEEOF
 9 <130> FILE REFERENCE: CLFR:007US
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/074,596
 12 <141> CURRENT FILING DATE: 2002-02-12
 14 <150> PRIOR APPLICATION NUMBER: 60/268,402
 15 <151> PRIOR FILING DATE: 2001-02-12
 17 <160> NUMBER OF SEQ ID NOS: 11
 19 <170> SOFTWARE: PatentIn Ver. 2.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 316
 23 <212> TYPE: PRT
 24 <213> ORGANISM: Gelonium multiflorum
 26 <400> SEQUENCE: 1
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 28 1 5 10 15
 30 Trp Phe Cys Cys Thr Thr Ile Val Leu Gly Ser Thr Ala Arg Ile Phe
 31 20 25 30
 33 Ser Leu Pro Thr Asn Asp Glu Glu Thr Ser Lys Thr Leu Gly Leu
 34 35 40 45
 36 Asp Thr Val Ser Phe Ser Thr Lys Gly Ala Thr Tyr Ile Thr Tyr Val
 37 50 55 60
 39 Asn Phe Leu Asn Glu Leu Arg Val Lys Leu Lys Pro Glu Gly Asn Ser
 40 65 70 75 80
 42 His Gly Ile Pro Leu Leu Arg Lys Lys Cys Asp Asp Pro Gly Lys Cys
 43 85 90 95
 45 Phe Val Leu Val Ala Leu Ser Asn Asp Asn Gly Gln Leu Ala Glu Ile
 46 100 105 110
 48 Ala Ile Asp Val Thr Ser Val Tyr Val Val Gly Tyr Gln Val Arg Asn
 49 115 120 125
 51 Arg Ser Tyr Phe Phe Lys Asp Ala Pro Asp Ala Ala Tyr Glu Gly Leu
 52 130 135 140
 54 Phe Lys Asn Thr Ile Lys Thr Arg Leu His Phe Gly Gly Ser Tyr Pro
 55 145 150 155 160
 57 Ser Leu Glu Gly Glu Lys Ala Tyr Arg Glu Thr Thr Asp Leu Gly Ile
 58 165 170 175
 60 Glu Pro Leu Arg Ile Gly Ile Lys Lys Leu Asp Glu Asn Ala Ile Asp
 61 180 185 190
 63 Asn Tyr Lys Pro Thr Glu Ile Ala Ser Ser Leu Leu Val Val Ile Gln
 64 195 200 205
 66 Met Val Ser Glu Ala Ala Arg Phe Thr Phe Ile Glu Asn Gln Ile Arg

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67	210	215	220
69	Asn Asn Phe Gln Gln Arg Ile Arg Pro Ala Asn Thr Ile Ser Leu		
70	225	230	235
72	Glu Asn Lys Trp Gly Lys Leu Ser Phe Gln Ile Arg Thr Ser Gly Ala		240
73	245	250	255
75	Asn Gly Met Phe Ser Glu Ala Val Glu Leu Glu Arg Ala Asn Gly Lys		
76	260	265	270
78	Lys Tyr Tyr Val Thr Ala Val Asp Gln Val Lys Pro Lys Ile Ala Leu		
79	275	280	285
81	Leu Lys Phe Val Asp Lys Asp Pro Lys Thr Ser Leu Ala Ala Glu Leu		
82	290	295	300
84	Ile Ile Gln Asn Tyr Glu Ser Leu Val Gly Phe Asp		
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88 <210> SEQ ID NO: 2

89 <211> LENGTH: 1176

90 <212> TYPE: DNA

91 <213> ORGANISM: *Gelonium multiflorum*

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 96 ctcttccac aaatgatgaa gaagaaacca gtaagacgct tggcctggac accgtgagct 180
 97 ttagcactaa aggtgccact tatattacct acgtgaattt cttgaatgag ctacgagtt 240
 98 aattgaaacc cgaaggtaac agccatgaa tccattgtct gcgcaaaaaa tgtgatgatc 300
 99 ctggaaagtg ttctgttttg gtagcgctt caaatgacaa tggacagttt gcccggaaatag 360
 100 ctatagatgt tacaagtgtt tatgtgtgg gctatcaagt aagaaacaga tcttacttct 420
 101 ttaaaagatgc tccagatgct gcttacaag gcttcttcaa aaacacaatt aaaacaagac 480
 102 ttcatttgg cggcagctat ccctcgctgg aaggtgagaa ggcataataga gagacaacag 540
 103 acttggccat tgaaccatta aggattggca tcaagaaact ttagaaaat ggcataatgc 600
 104 attataaacc aacggagata gctagtttc tattggttgt tattcaatg gtgtctgaag 660
 105 cagctcgatt cacctttatt gagaacaaa tttagaaataa ctttcaacag agaattcgcc 720
 106 cggcgaataa tacaatcago ttggagaata aatggggtaa actctcggtc cagatccgga 780
 107 catcagggtgc aaatggaatg tttcggagg cagttgaattt ggaacgtgca aatggcaaaa 840
 108 aataactatgt caccgcagtt gatcaagtaa aacccaaaat agcactctt aagttcgctc 900
 109 ataaagatcc taaaacgagc cttgctgct aattgataat ccagaactat gagtcatat 960
 110 tgggcttga tttagtacaac ttattgtgt ttttatatat tatagatatg atgccgggccc 1020
 111 atgtattggc cttcgtagct taaataaagg catgaatat tagcctcggt ggtgtatcta 1080
 112 tcatgctgtg ttgtaaaact gccaatgttt atgttatcaa acagaaattt gcatgaagtt 1140
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116 <210> SEQ ID NO: 3

117 <211> LENGTH: 33

118 <212> TYPE: DNA

119 <213> ORGANISM: *Homo sapiens*

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126 <211> LENGTH: 50

127 <212> TYPE: DNA

128 <213> ORGANISM: *Homo sapiens*

130 <400> SEQUENCE: 4

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137 <213> ORGANISM: Homo sapiens
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144 <211> LENGTH: 30
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146 <213> ORGANISM: Homo sapiens
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155 <213> ORGANISM: Artificial Sequence
157 <220> FEATURE:
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184 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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193 <212> TYPE: DNA
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196 <220> FEATURE:
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199 <220> FEATURE:
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201 <222> LOCATION: (1)..(1521)

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206	1							5		10					15		
208	gta	gga	gac	agg	gtc	agc	gtc	acc	tgc	aag	gcc	agt	cag	aat	gtg	gat	96
209	Val	Gly	Asp	Arg	Val	Ser	Val	Thr	Cys	Lys	Ala	Ser	Gln	Asn	Val	Asp	
210								20		25			30				144
212	act	aat	gta	gcc	tgg	tat	caa	caa	aaa	cca	ggg	caa	tct	cct	gaa	cca	
213	Thr	Asn	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Glu	Pro	
214							35		40			45					192
216	ctg	ctt	ttc	tcg	gca	tcc	tac	cgt	tac	act	gga	gtc	cct	gat	cgc	ttc	
217	Leu	Leu	Phe	Ser	Ala	Ser	Tyr	Arg	Tyr	Thr	Gly	Val	Pro	Asp	Arg	Phe	
218							50		55		60						240
220	aca	ggc	agt	gga	tct	ggg	aca	gat	ttc	act	ctc	acc	atc	agc	aat	gtg	
221	Thr	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Asn	Val	
222							65		70		75			80			288
224	cag	tct	gaa	gac	ttg	gca	gag	tat	ttc	tgt	cag	caa	tat	aac	agc	tat	
225	Gln	Ser	Glu	Asp	Leu	Ala	Glu	Tyr	Phe	Cys	Gln	Gln	Tyr	Asn	Ser	Tyr	
226							85		90		95						336
228	cct	ctg	acg	ttc	ggg	gga	ggc	acc	aag	ctg	gag	atc	aaa	ggc	tcc	acc	
229	Pro	Leu	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Gly	Ser	Thr	
230							100		105		110						384
232	agc	ggc	agc	ggt	aag	cca	ggc	tcc	ggc	gaa	ggc	agc	acc	aaa	ggc	gaa	
233	Ser	Gly	Ser	Gly	Lys	Pro	Gly	Ser	Gly	Glu	Gly	Ser	Thr	Lys	Gly	Glu	
234						115		120		125							432
236	gtg	aag	gtt	gag	gag	tct	gga	gga	ggc	ttg	gtg	caa	cct	gga	gga	tcc	
237	Val	Lys	Val	Glu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	
238						130		135		140							480
240	atg	aaa	ctc	tcc	tgt	gtt	gtc	tct	gga	ttc	act	ttc	gtt	aat	tac	tgg	
241	Met	Lys	Leu	Ser	Cys	Val	Val	Ser	Gly	Phe	Thr	Phe	Gly	Asn	Tyr	Trp	
242						145		150		155		160					528
244	atg	aac	tgg	gtc	cgc	cag	tct	cca	gag	aag	ggg	ctt	gag	tgg	att	gca	
245	Met	Asn	Trp	Val	Arg	Gln	Ser	Pro	Glu	Lys	Gly	Leu	Glu	Trp	Ile	Ala	
246						165		170		175							576
248	gaa	att	aga	ttg	aaa	tcc	aat	aat	ttt	gca	aga	tat	tat	gcg	gag	tct	
249	Glu	Ile	Arg	Leu	Lys	Ser	Asn	Asn	Phe	Ala	Arg	Tyr	Tyr	Ala	Glu	Ser	
250						180		185		190							624
252	gtg	aaa	ggg	agg	ttc	acc	atc	tca	aga	gat	gat	tcc	aaa	agt	agt	gtc	
253	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	Ser	Ser	Val	
254						195		200		205							672
256	tac	ctg	caa	atg	atc	aac	cta	aga	gct	gaa	gat	act	ggc	att	tat	tac	
257	Tyr	Leu	Gln	Met	Ile	Asn	Leu	Arg	Ala	Glu	Asp	Thr	Gly	Ile	Tyr	Tyr	
258						210		215		220							720
260	tgt	acc	agt	tat	ggt	aac	tac	gtt	ggg	cac	tat	ttt	gac	cac	tgg	ggc	
261	Cys	Thr	Ser	Tyr	Gly	Asn	Tyr	Val	Gly	His	Tyr	Phe	Asp	His	Trp	Gly	
262						225		230		235		240					768
264	caa	ggc	acc	act	ctc	acc	gtc	tcc	tca	gct	agc	ggg	gtt	ggc	ggc	tcc	
265	Gln	Gly	Thr	Thr	Leu	Thr	Val	Ser	Ser	Ala	Ser	Gly	Gly	Gly	Ser		
266						245		250		255							

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268	ggt cta gac acc gtg agc ttt agc act aaa ggt gcc act tat att acc	816
269	Gly Leu Asp Thr Val Ser Phe Ser Thr Lys Gly Ala Thr Tyr Ile Thr	
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272	tac gtg aat ttc ttg aat gag cta cga gtt aaa ttg aaa ccc gaa ggt	864
273	Tyr Val Asn Phe Leu Asn Glu Leu Arg Val Lys Leu Lys Pro Glu Gly	
274	275 280 285	
276	aac agc cat gga atc cca ttg ctg cgc aaa aaa tgt gat gat cct gga	912
277	Asn Ser His Gly Ile Pro Leu Leu Arg Lys Lys Cys Asp Asp Pro Gly	
278	290 295 300	
280	aag tgt ttc gtt ttg gta gcg ctt tca aat gac aat gga cag ttg gcg	960
281	Lys Cys Phe Val Leu Val Ala Leu Ser Asn Asp Asn Gly Gln Leu Ala	
282	305 310 315 320	
284	gaa ata gct ata gat gtt aca agt gtt tat gtg gtg ggc tat caa gta	1008
285	Glu Ile Ala Ile Asp Val Thr Ser Val Tyr Val Val Gly Tyr Gln Val	
286	325 330 335	
288	aga aac aga tct tac ttc ttt aaa gat gct cca gat gct gct tac gaa	1056
289	Arg Asn Arg Ser Tyr Phe Phe Lys Asp Ala Pro Asp Ala Ala Tyr Glu	
290	340 345 350	
292	ggc ctc ttc aaa aac aca att aaa aca aga ctt cat ttt ggc ggc agc	1104
293	Gly Leu Phe Lys Asn Thr Ile Lys Thr Arg Leu His Phe Gly Gly Ser	
294	355 360 365	
296	tat ccc tcg ctg gaa ggt gag aag gca tat aga gag aca aca gac ttg	1152
297	Tyr Pro Ser Leu Glu Gly Glu Lys Ala Tyr Arg Glu Thr Thr Asp Leu	
298	370 375 380	
300	ggc att gaa cca tta agg att ggc atc aag aaa ctt gat gaa aat gcg	1200
301	Gly Ile Glu Pro Leu Arg Ile Gly Ile Lys Lys Leu Asp Glu Asn Ala	
302	385 390 395 400	
304	ata gac aat tat aaa cca acg gag ata gct agt tct cta ttg gtt gtt	1248
305	Ile Asp Asn Tyr Lys Pro Thr Glu Ile Ala Ser Ser Leu Leu Val Val	
306	405 410 415	
308	att caa atg gtg tct gaa gca gct cga ttc acc ttt att gag aac caa	1296
309	Ile Gln Met Val Ser Glu Ala Ala Arg Phe Thr Phe Ile Glu Asn Gln	
310	420 425 430	
312	att aga aat aac ttt caa cag aga att cgc ccg gcg aat aat aca atc	1344
313	Ile Arg Asn Asn Phe Gln Gln Arg Ile Arg Pro Ala Asn Asn Thr Ile	
314	435 440 445	
316	agc ctt gag aat aaa tgg ggt aaa ctc tcg ttc cag atc cgg aca tca	1392
317	Ser Leu Glu Asn Lys Trp Gly Lys Leu Ser Phe Gln Ile Arg Thr Ser	
318	450 455 460	
320	ggt gca aat gga atg ttt tcg gag gca gtt gaa ttg gaa cgt gca aat	1440
321	Gly Ala Asn Gly Met Phe Ser Glu Ala Val Glu Leu Glu Arg Ala Asn	
322	465 470 475 480	
324	ggc aaa aaa tac tat gtc acc gca gtt gat caa gta aaa ccc aaa ata	1488
325	Gly Lys Lys Tyr Tyr Val Thr Ala Val Asp Gln Val Lys Pro Lys Ile	
326	485 490 495	
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329	Ala Leu Leu Lys Phe Val Asp Lys Asp Pro Lys	
330	500 505	
333	<210> SEQ ID NO: 11	

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